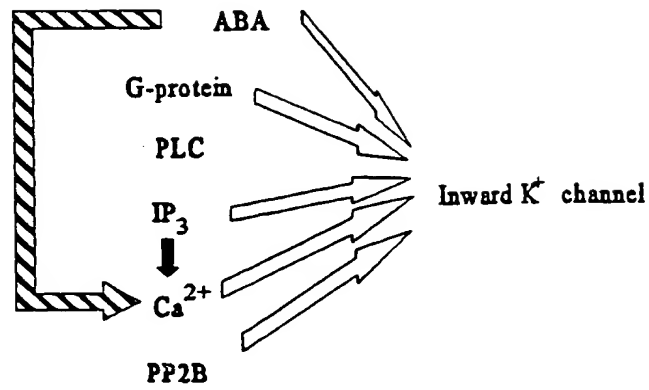


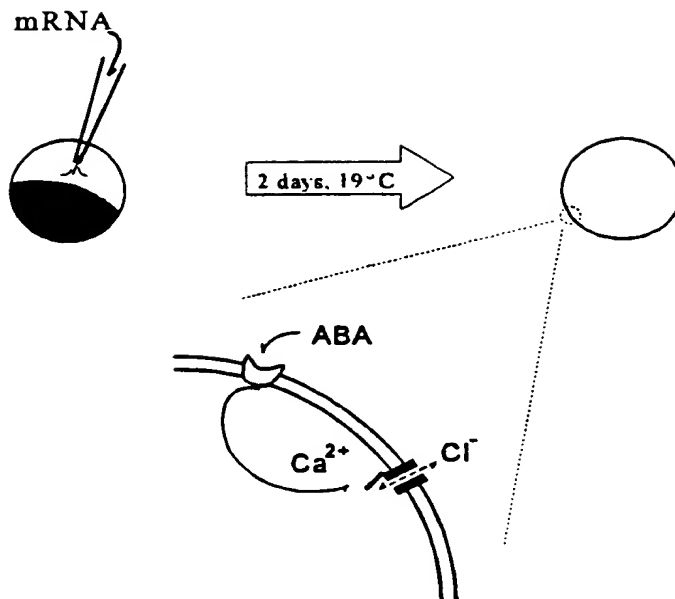
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FIG. 1



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A.



B.

Sucrose gradient fractionation

cDNA library construction

Pool and subdivide

Transcribe pools separately
with T7 polymerase

Assay and select positives

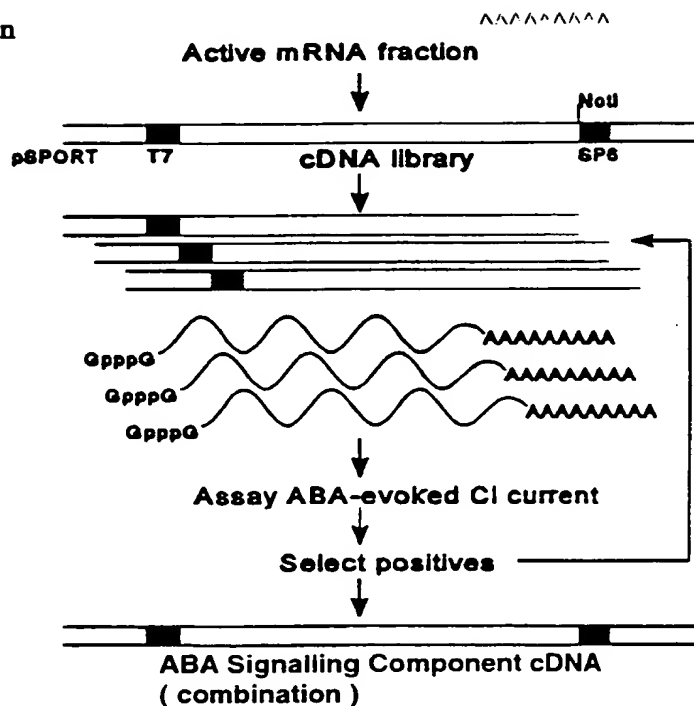


FIG. 2

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A.

1	S	N	P	E	E	K	E	F	L	D	W	S	K	R	V	I	I	E	G	I	G	R	G	L	L	Y	L	H	R	D	REK-Nt (5' end)	
620	N	K	-	Q	R	S	S	L	L	N	W	Q	T	R	F	N	I	I	C	G	I	A	R	G	L	L	Y	L	H	Q	D	IRK1-It
621	-	-	-	-	-	-	-	-	L	N	W	K	D	R	F	A	I	T	N	G	V	A	R	G	L	L	Y	L	H	Q	D	SRK9-Bc
616	K	K	-	-	R	S	S	N	L	N	W	K	D	R	F	A	I	T	N	G	V	A	R	G	L	L	Y	L	H	Q	D	SRK4-Bo

32	S	R	L	R	I	I	H	R	D	L	K	A	S	N	I	L	L	D	E	Q	L	N	P	K	I	S	D	F	G	M	A	REK-Nt (5' end)
650	S	R	F	R	I	I	H	R	D	L	K	A	S	N	I	L	L	D	K	E	M	N	P	K	I	S	D	F	G	M	A	IRK1-It
644	S	R	F	R	I	I	H	R	D	L	K	P	G	N	I	L	L	D	K	Y	M	I	P	K	I	S	D	F	G	M	A	SRK9-Bc
645	S	R	F	R	I	I	H	R	D	M	K	P	S	N	I	L	L	D	K	Y	M	I	P	K	I	S	D	F	G	M	A	SRK4-Bo

63	R	I	F	P	G	S	Q	D	Q	A	N	T	E	R	V	V	G	T	REK-Nt (5' end)
681	R	I	F	G	G	D	E	T	D	A	N	N	T	K	R	V	C	IRK1-It	
675	R	I	F	A	R	D	E	I	Q	A	R	T	D	N	A	V	G	T	SRK9-Bc
676	R	I	F	A	R	D	E	T	E	A	N	T							SRK4-Bo

B.

1	G	L	L	C	V	Q	E	Y	A	E	D	R	P	N	V	S	V	L	S	M	L	T	S	E	I	S	D	L	P	S	REK-Nt (3' end)	
784	G	L	L	C	V	Q	E	Q	A	E	D	R	P	N	M	A	T	V	V	L	M	L	G	S	E	S	A	T	L	P	Q	IRK1-It
784	G	L	L	C	I	Q	E	R	A	E	H	R	P	T	M	S	S	V	V	W	M	L	G	S	E	A	T	E	I	P	Q	SRK9-Bc
785	G	L	L	C	I	Q	E	R	A	E	D	R	P	T	M	S	S	V	V	W	M	L	G	S	E	A	T	D	I	P	Q	SRK4-Bo

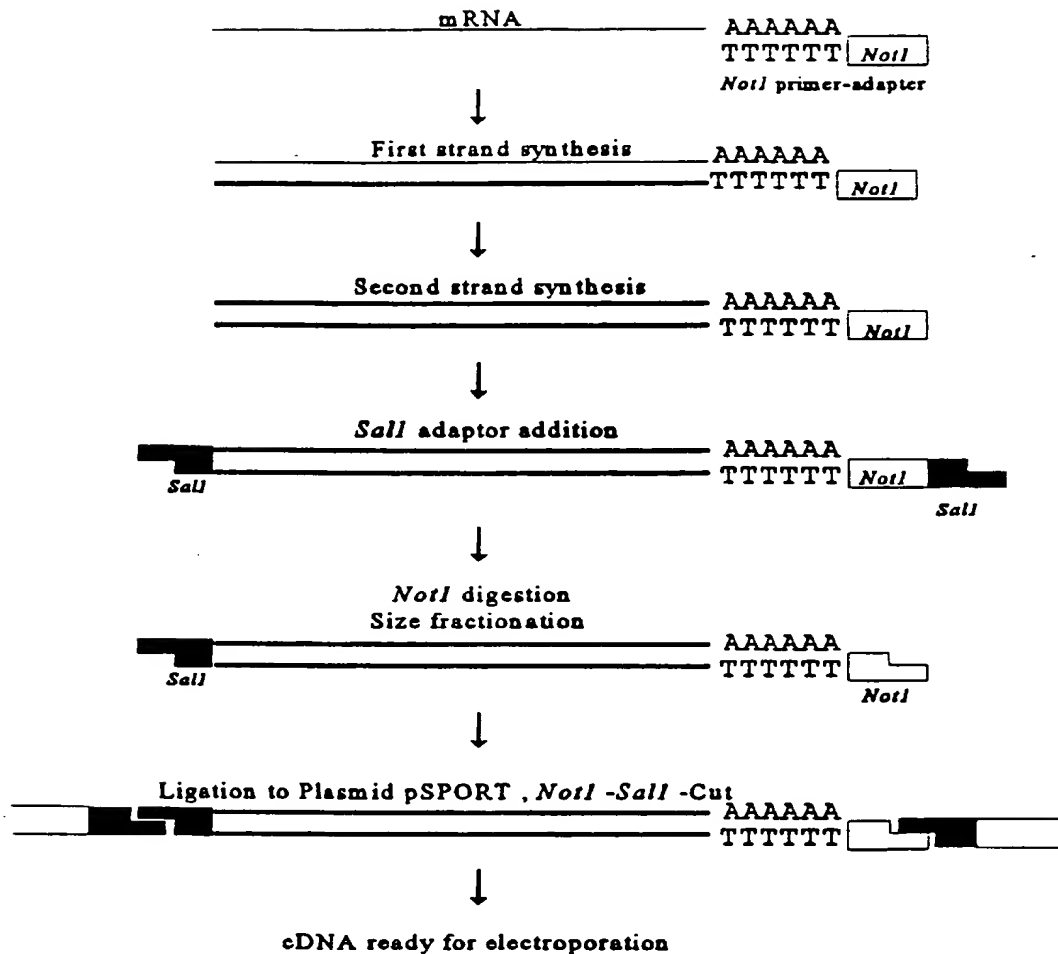
32	P	K	Q	F	A	F	T	T	R	P	S	C	S	E	K	E	S	S	K	T	Q	-	-	-	-	-	-	-	-	-	SV	REK-Nt (3' end)	
815	P	K	H	P	G	F	C	L	G	S	R	P	A	D	M	D	S	S	T	S	-	N	C	D	E	S	C	-	-	-	T	V	IRK1-It
815	P	K	P	P	V	Y	C	L	I	A	S	Y	Y	A	N	N	P	S	S	S	R	Q	F	D	D	D	E	S	W	T	V	SRK9-Bc	
816	P	K	P	P	I	Y	C	L	I	T	S	Y	Y	A	N	N	P	S	S	S	R	Q	F	E	D	D	E	S	W	T	V	SRK4-Bo	

56	N	T	V	S	I	F	I	M	E	G	R																				REK-Nt (3' end)
843	N	Q	V	T	V	T	M	L	D	G	R																				IRK1-It
846	D	K	Y	T	W	S	V	I	D	A	R																				SRK9-Bc
847	N	K	Y	T	C	S	V	I	D	A	R																				SRK4-Bo

FIG. 3

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A.



B.

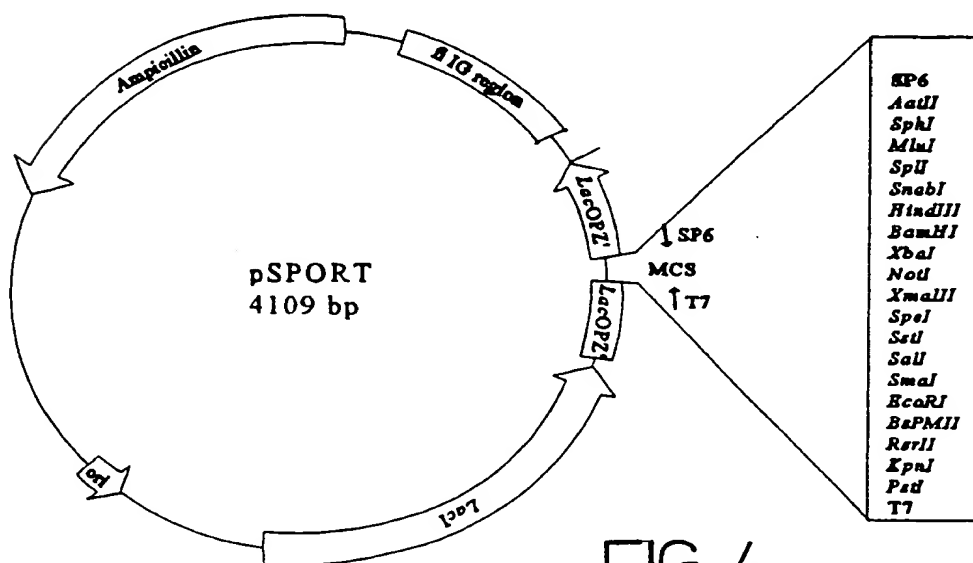


FIG. 4

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11 L I F S L E T F L L V L L F F T L V S S S A S E I F F E E S F D D G CAL-tN (5'end)
 6 N K L S F F C F F F L V S V L T L A P L A F S E I F L E E H F E G G CRT1-At
 45 W R S R W V R S D W K I S E G K A G S F K H T A G T W A G D P D D K CAL-tN (5'end)
 40 W K S R W V L S D W K R N E G K A G T F K H T A G K W P G D P D N K CRT1-At
 79 G I H T T N D A K H F A V S A K I P E F S N K N R T L V V Q Y S I K CAL-tN (5'end)
 74 G I Q T Y N D A K H Y A I S A K I P E F S N K N R T L V V Q Y S V K CRT1-At
 113 F E P D I E C G R G Y I K L L S G Y V H P K K F G G D T P Y S F M F CAL-tN (5'end)
 108 I E Q D I E C G G A Y I K L L S G Y V N Q K Q F G G D T P Y S L M F CRT1-At
 147 G A D I C G S Q T R K K P S C L Y F F Y P G A E L P P L P E R N L CAL-tN (5'end)
 142 G P D I C G T Q T K K L H - V I V S Y Q G Q N Y P I - - K K D L CRT1-At

A

1 G V W M - - E P D I A R T S D S R K C L P I G E A E K E A F E E A E CAL-Nt (3'end)
 340 - I L I C D D P A Y A R S I V D D Y F A Q H R E S E K E L F A E A E CRT1-At
 33 K V R K A R E E E E A Q R A R E E G E R R K R E R G R - - D R A R D CAL-Nt (3'end)
 373 K E R K A R E D E E A R I A R E E G E R R R K E R D H R Y G D R R R CRT1-At
 65 R I K K K I H H D Y M D D Y H D E L CAL-Nt (3'end)
 407 R Y K R P N P R D Y M D D Y H D E L CRT1-At

B

FIG. 7

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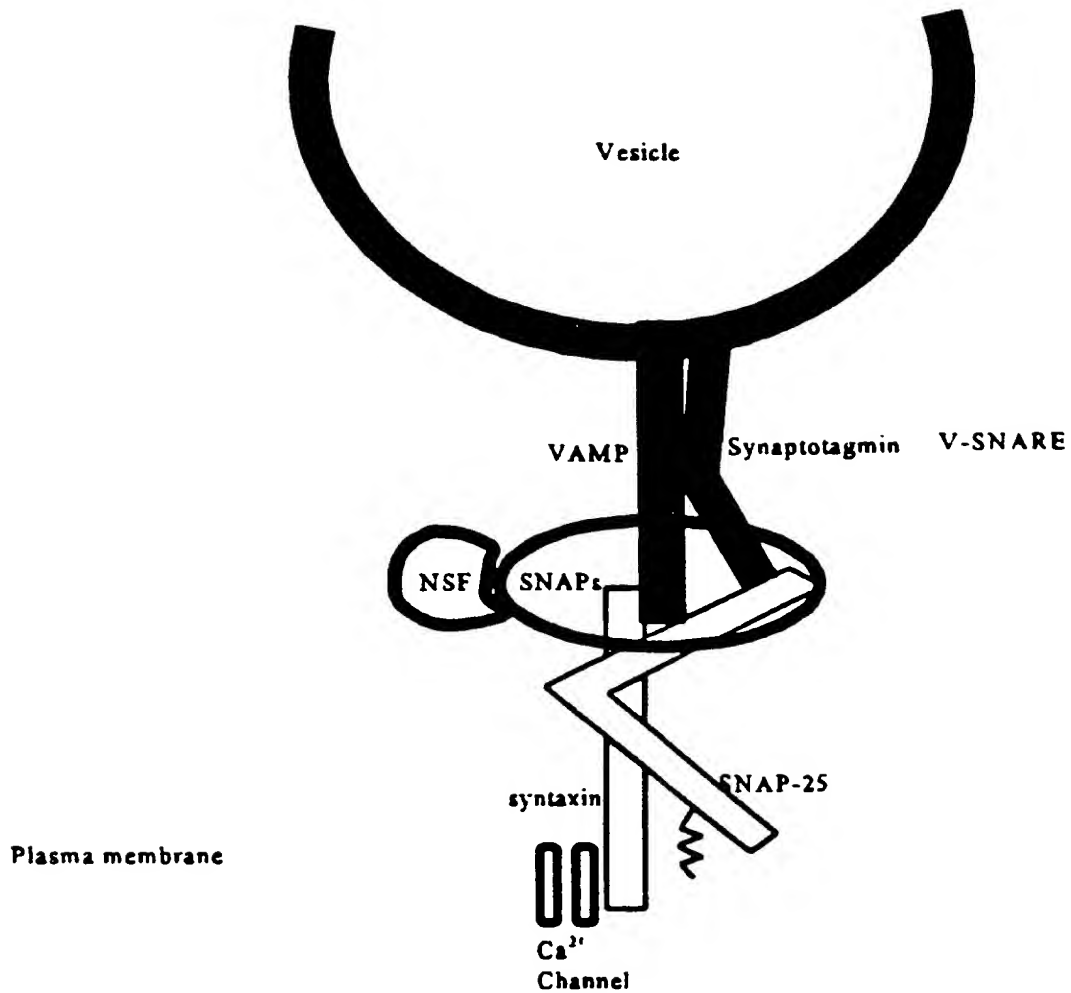
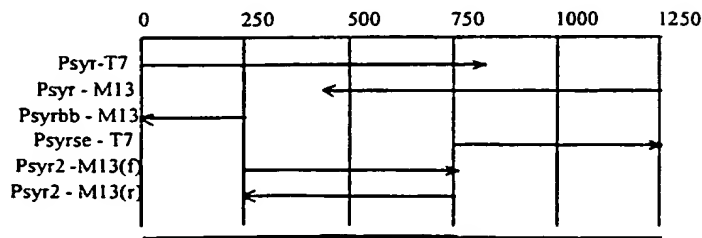


FIG. 8

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CCAAATCCCATCTCAAATGAATGATCTATTTTCAGGATCTTTCTCTCGTTTCAGAGCTG 60
M N D L F S G S F S R F R A
ACGATCAATCGGACTCTCACGCCATAGAAATGGGAGACATTACTGGCGGAGTCAATCTCG 120
D D Q S D S H A I E M G D I T G G V N L
ACAAATTCTTCGAAGATGTTGAAGCCATTAAAGACGAAGCTCAAAGGCCTCGAGAAAATCT 180
D K F F E D V E A I K D E L K G L E K I
ATTCCCAACTCCAATCTTCCCATGAAAAAGCAAGACTCTTCAACGCTAAAGCCGTTA 240
Y S Q L Q S S H E K S K T L H N A K A V
AAGATCTAAGATCCAACATGGATAATGACGTTTCCATGGCATTGAAGAAAGCCAAATTCA 300
K D L R S N M D N D V S M A L K K A K F
TCAAAGTTCGTCTCGAAGCCTTAGACAGATCAAATGCAGCGAATCGAAGCCTCCCTGGAT 360
I K V R L E A L D R S N A A N R S L P G
GTGGACCCGGAAGTTCATCTGACAGGACGAGAAGTTCAGTTGTGAACGGATTAAGGAAGA 420
C G P G S S S D R T R T S V V N G L R K
AACTTCAAGAGTCAATGAATCAGTTCAACGAGCTAAGGCAAAAGATGGCATCTGAATATA 480
K L Q E S M N Q F N E L R Q K M A S E Y
GGGAAACAGTTCAACGACGATATTATACCGTCACAGGAGAAAAATCCTGATGAAGCAGTTC 540
R E T V Q R R Y Y T V T G E N P D E A V
TTGATACACTCATATCTACAGGTCAAAGTGAGACGTTCTTGCAAAAGGCAATTCAAGAGC 600
L D T L I S T G Q S E T F L Q K A I Q E
AAGGGAGAGGACAAGTGATGGATACAGTTATGGAAATTCAGAAAGGCATGAAGCTGTGA 660
Q G R G Q V M D T V M E I Q E R H E A V
AGGAATGGAGAGGAATTTGAAAGAATTGCATCAAGTATTCTTGGACATGGCTGTTTGG 720
K E L E R N L K E L H Q V F L D M A V L
TTGAAAGTCAAGGAGCTCAACTTGATGATATTGAGAGCCAAGTGAATAGGGCTAATTCCT 780
V E S Q G A Q L D D I E S Q V N R A N S
TCGTTAGAGGGGGTGCTCAGCAACTGCAAGTGGCAAGGAAGCACCAGAAGAACTAGAA 840
F V R G G A Q Q L Q V A R K H Q K N T R
AATGGACTTGTTTTGCTATTATTCTTCTGCTTATCATCATTTTGGTGGTGGTTCTTTCTA 900
K W T C F A I I L L L I I I L V V V L S
TTCAGCCATGGAAAAATGAGAAATTTGTCTATGGTCAAAGGTCTTCTGGTGGACCCCTTC 960
I Q P W K K
AATGTTTTGAATATTCTAAATTTTTATTTTTATTATTTTAGCCATGCTTATTATTTTGT 1020
GTTATTTTGGATTTTTTTTTTGTGTTTAAATGTGGGGAAGAGTAAACTGGATGGGGGTCCA 1080
TGTGCTATTTAGAGAAATACTTGGGAGTTCTCTTTTTGTAAATTATTGCTGTATTTAGAGT 1140
ATAATCTTTTTCTATATTGTTGGCAGGTTAATTGTTTGTGTTGATTATATCTCATTTA 1200
GATT 1205

A



B

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1 MNDLFSGSFSRFRADDOQSDSHAIEMG-----DITGGV SYNTAXIN.PRO
1 MNDLMTKSEMSYVDLKKAAAMKDM EAGPFDLEMASTRACHMDEND KNOLLE.PRO
1 M-----SYNAHUM.PRO
1 M-F-----DRTQVLRIRRNNSDDKEEVVHV-----RIRH SYNBHUM.PRO
1 MTK-----DRLAALHAQAQSDDEEETEVAVNV-----GHDS SYNADRO.PRO

33 NLDKFFEDDEAIAIKDELKGLENIYSLLSSHEKSRITLHNAKAVRDL SYNTAXIN.PRO
46 DLSSEFLFEAEYVKAEMJLISETLARIEQYHEESKGVHKAESVXS L KNOLLE.PRO
2 -LEFFEEQVEEIR--GFIDIAENVVEYKRKHSALASPNPDERK SYNAHUM.PRO
28 FMDEFFEEQEEEIR--GCIEHLSSEVDVQVKKQHSALAPNPER SYNBHUM.PRO
30 YMDDEFFAQVEEIR--GMIDKVCNVVEYVKKKHSALASAPCTDERK SYNADRO.PRO

75 RSNMMDNEVSMALRAAK--FIRVVKLEALERSRAANASLFSGDFSS SYNTAXIN.PRO
81 RNKISNEIYSGLRKDOAKSISKSKLEEMKANKKEIKRL--SSTF KNOLLE.PRO
42 TKVELEELMSDIKKTANK-VRSKLKSEIEQSIEQEEGL--HRS SA SYNAHUM.PRO
70 TKQELEELTADIKKTANK-VRSKLKAIIEQSIEQEEGS--TAPRP SYNBHUM.PRO
74 TKQELEELMADIKKNANR-VRGKLKGIEQNIIEQEEQQ--NKS SA SYNADRO.PRO

121 SDAKTKTSTVNGLRKKLQESHNLFHELRQKM--ASEKRETQRYRY- SYNTAXIN.PRO
132 VYRSRTAVTNGLRKKLKEVMMEFQGLRQKMMSEDDYKETVERRY- KNOLLE.PRO
93 DLRIIRKTQHSTLSRKFFVEVMSEYHA--TQSVYKRECKGRIQ SYNAHUM.PRO
111 ILRIIRKTQHSTLSRKFFVEVMTEYHA--TQSKYRDRCKDRIQ SYNBHUM.PRO
115 DLRIIRKTQHSTLSRKFFVEVMTEYHR--TQTDYKRECKGRIQ SYNADRO.PRO

163 --YTVFGENPDEAVLETLISTQS-ETLQKAQEQRGQVMDTV SYNTAXIN.PRO
176 --FTVTGEHANDEMIKIIITDNAGGEEFLTRAIQEHGKGHVLTV KNOLLE.PRO
122 RQLEITGRTTTSEELDMLESUNPA-IFASGIIMDSSISH--QAL SYNAHUM.PRO
150 RQLEITGRTTTNEELEDMLESGLKP-IFTDDIKMDSQMTB--QAL SYNBHUM.PRO
154 RQLEITGRTPTNDDELEKMLEEGNS-S-VFTQGI-METQQAAR--QTL SYNADRO.PRO

205 MEIQSRHE--AVRELERHKLKELHQVFLDMHAVLVESQGAQLLEILS SYNTAXIN.PRO
219 VEIQSRQYDAAKEIEKSLLELHQVFLDMAVMVESQGEQMDIEIEH KNOLLE.PRO
164 SEIETRH--SEIIKLENSIRELHDMFMDMAMLVESQGEIMICRIEY SYNAHUM.PRO
192 NEIETRH--NEIIKLETSIRELHDMFVDMAMLVESQGEIMIDRIEY SYNBHUM.PRO
196 AQIEARH--QDIMKLETSIKELHDMFMDMAMLVESQGEIMIDRIEY SYNADRO.PRO

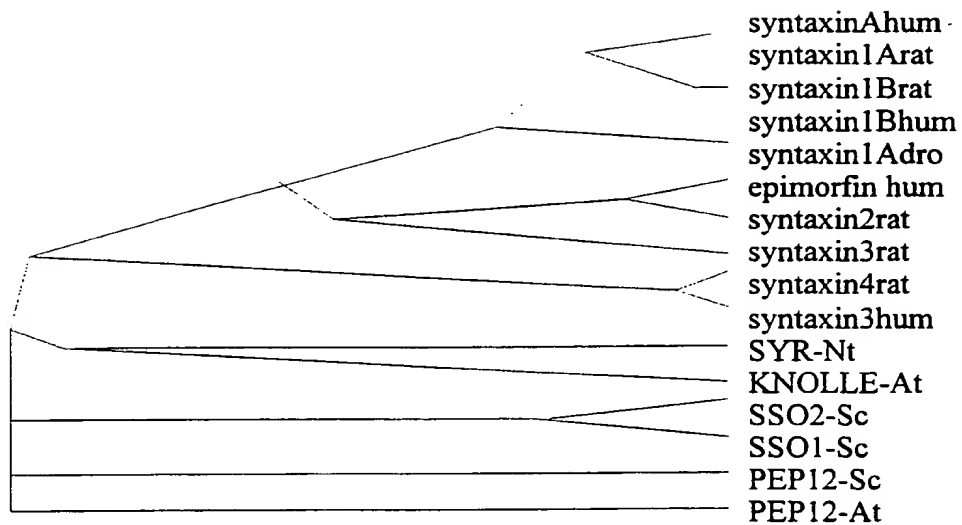
248 QVNRANSFVRGGAQQQLQVA--RHHKMTAKWTCFALILLLLIIEV SYNTAXIN.PRO
264 HVINASHYVADGANELTASDOHHRNSAKWMCQIIVLLLIILIT KNOLLE.PRO
207 NVEHAVDYVERAVSDT--FAVRYQSKAKRKK--MIIICCVILGI SYNAHUM.PRO
235 NVEHSVDYVERAVSDT--FAVRYQSKAKRKK--MIIICCVVLGV SYNBHUM.PRO
239 HVEHAMDYVQTATQDT--EALRYQSKAKRKK--MILICLTVLGI SYNADRO.PRO

291 VVLSTIQPW--KK SYNTAXIN.PRO
309 VVIPIITSFSS KNOLLE.PRO
249 VIASTVGGIFA SYNAHUM.PRO
277 VLASSIIGCTLGL SYNBHUM.PRO
281 LAASYVSSYF-M SYNADRO.PRO

FIG.10

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FIG 11



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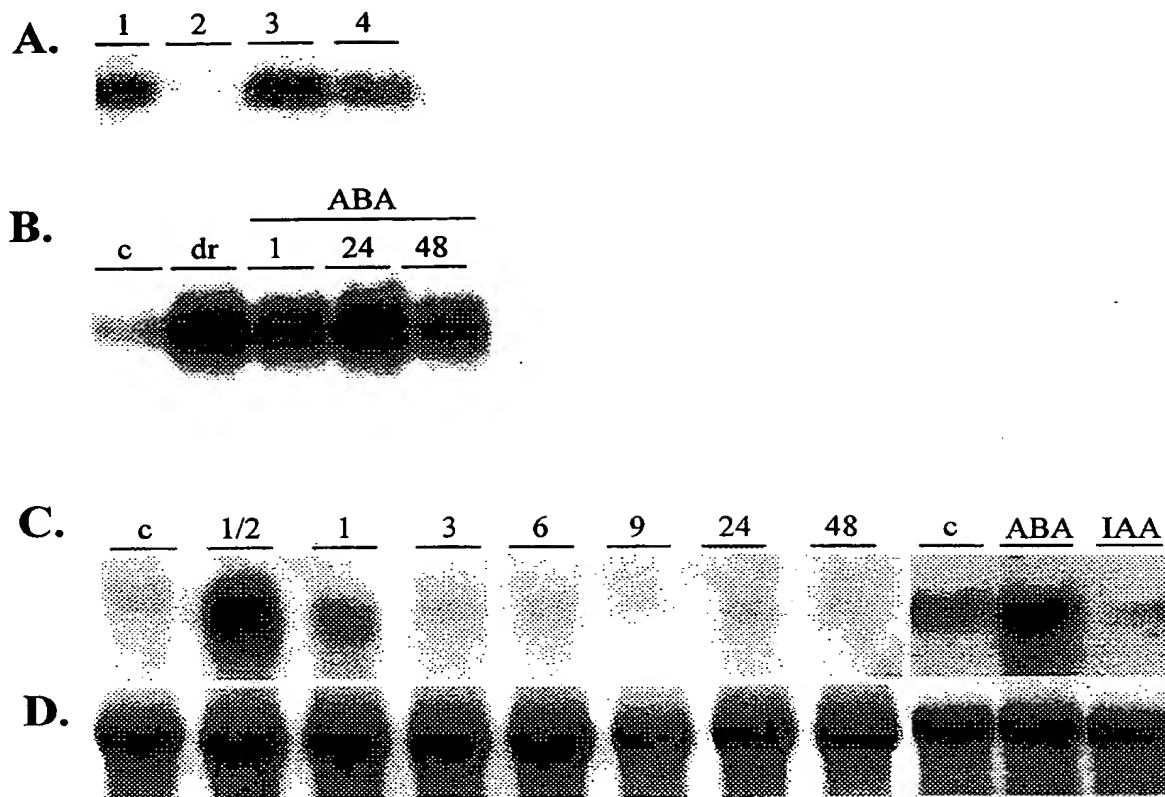


FIG. 12

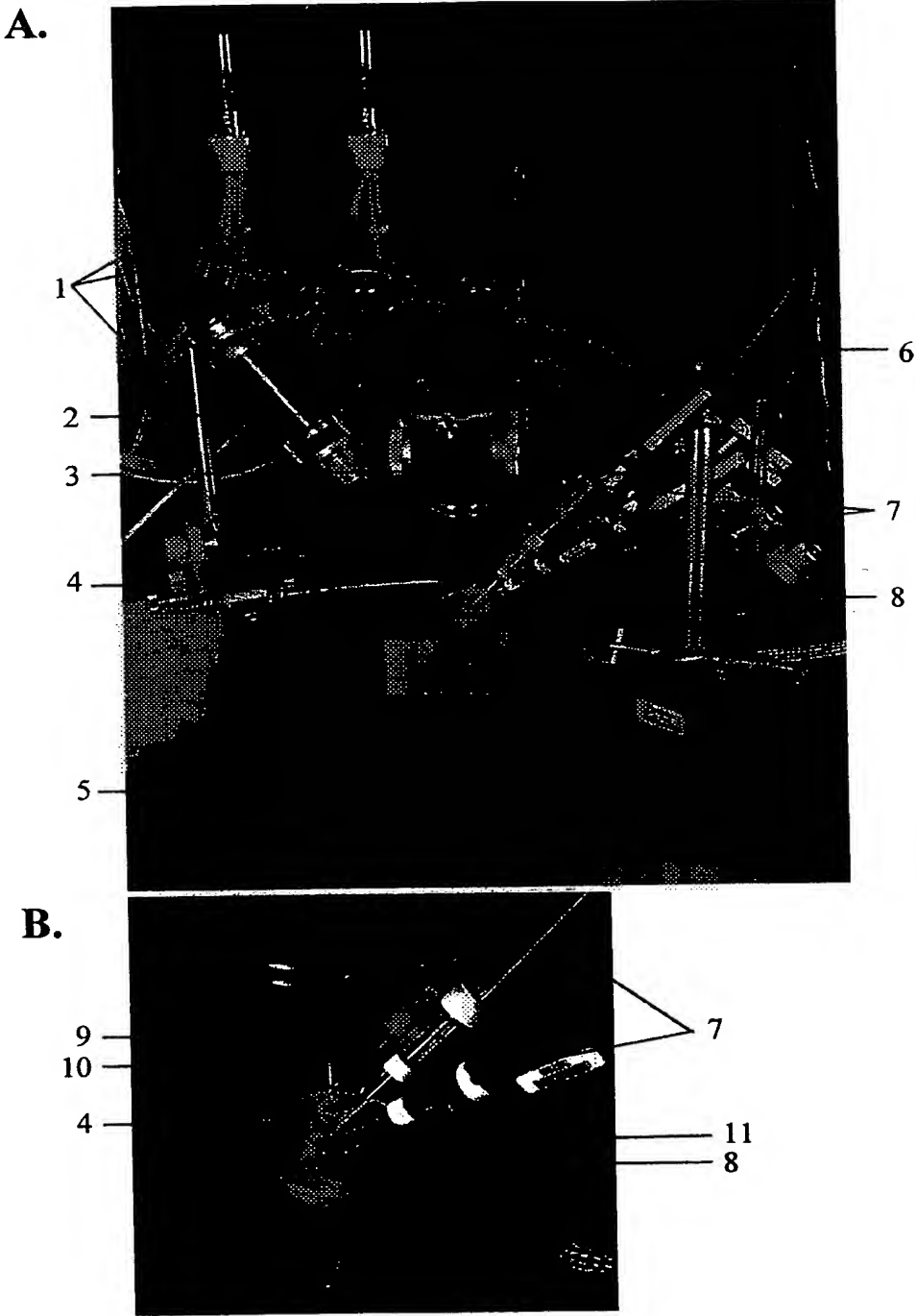


FIG. 13

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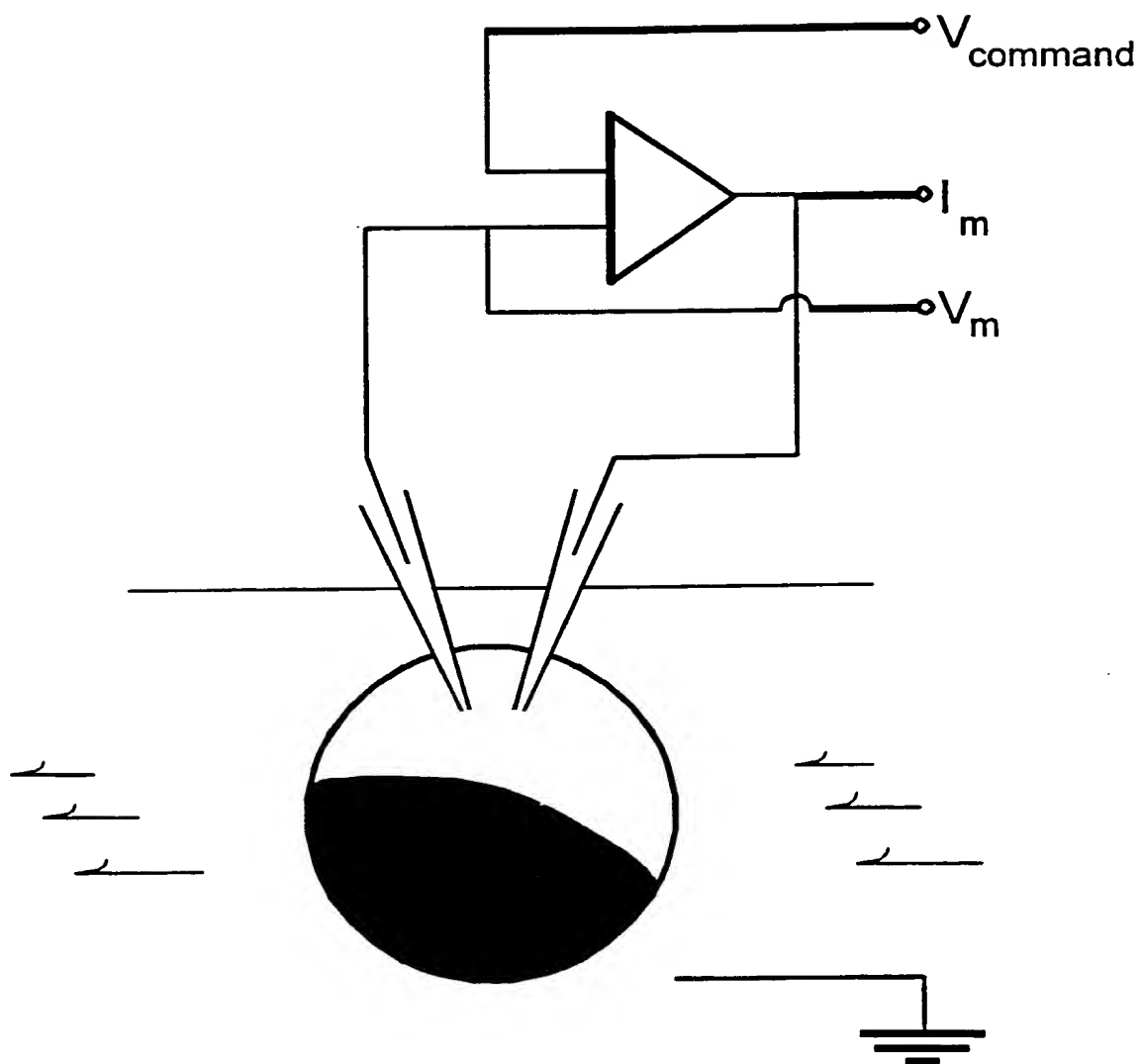


FIG. 14

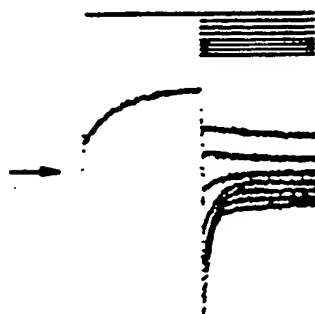
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A


30mM Cl^-

90mM Cl^-


B

90 mM Cl^- and 1 mM Ca^{2+}


C


10 mM Ca^{2+} (5min)

10 mM Ca^{2+} (10 min)


FIG.15

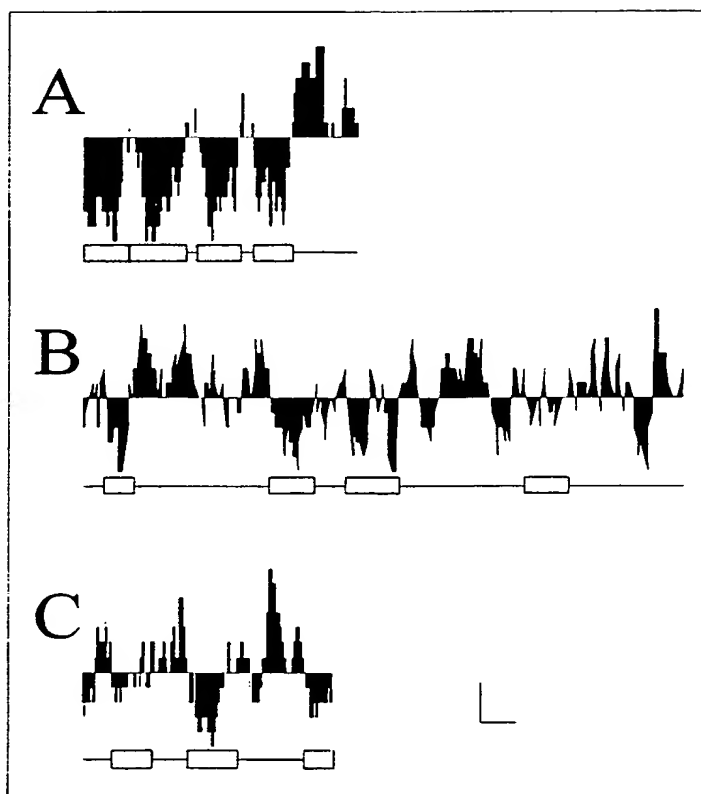
APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	WO 99/16880	

09/509738

PCT/GB98/02937

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FIG 5



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FIG. 6

17	R F R A V T S A Y Y R S A V G A L L V Y D I S R K T T F E N I	smG-Nt2
74	R F R A V T S A Y Y R G A V G A L I V Y D I S R R T T F D S V	Soybean
74	R F R A V T S A Y Y R G A V G A L I V Y D I T R R T T F D S V	L.Japonicus
74	R F R A V T S A Y Y R G A V G A L V V Y D I T R R T T F E S V	A. thaliana1
73	R F R A V T S A Y Y R G A V G A L V V Y D I T R S S T F E N V	A. thaliana2
65	R F R A V T S A Y Y R G A F G A L V V Y D I T R R T T F D S I	N.tabacum2
48	Q C W L D E L H T H C D T T V A R M L V G N K C D L E N I R D	smG-Nt2
105	G R W L D E L K T H C D T T V A M M L V G N K C D L E N I R A	Soybean
105	S R W L D E L K T H C D T T V A M M L V G N K C D L E N I R A	L.Japonicus
105	G R W L D E L K I H S D T T V A R M L V G N K C D L E N I R A	A. thaliana1
104	G R W L D E L N T H S D T T V A K M L I G N K C D L E S I R A	A. thaliana2
96	P R W L D E L K T H S D T T V A R M L V G N K C D L D N I R A	N.tabacum2
79	V S I Y E G K N L A E E E G L F F I E T S A L D S T N V K Q P	smG-Nt2
136	V S I D E G K S L A E A E G L F F M E T S A L D S T N V K M A	Soybean
136	V S I E E G K S L A E A Q G L F F M E T S A L D S T N V R T A	L.Japonicus
136	V S V E E G K A L A E E E G L F F V E T S A L D S T N V K T A	A. thaliana1
135	V S V E E G K S L A E S E G L F F M E T S A L D S T N V K T A	A. thaliana2
127	V S V E E G K S L A E S E G M F F M E T S A L D A T N V N K A	N.tabacum2
110	L K L S S A Q I Y Q N L S R K V L H S D S Y K T E L S V H P V	smG-Nt2
167	F E M V I R E I Y N N V S R K V L N S E T Y K A E L S V N R V	Soybean
167	F E M V I R E I Y N N V S R K V L N S D T Y K A E L S V D R V	L.Japonicus
167	F E M V I L D I Y N N V S R K Q L N S D T Y K D E L T V N R V	A. thaliana1
166	F E M V I R E I Y S N I S R K Q L N S D S Y K E E L T V N R V	A. thaliana2
158	F D M V I R E I Y N S V S R K V L N S D S Y K A E L S V N R V	N.tabacum2

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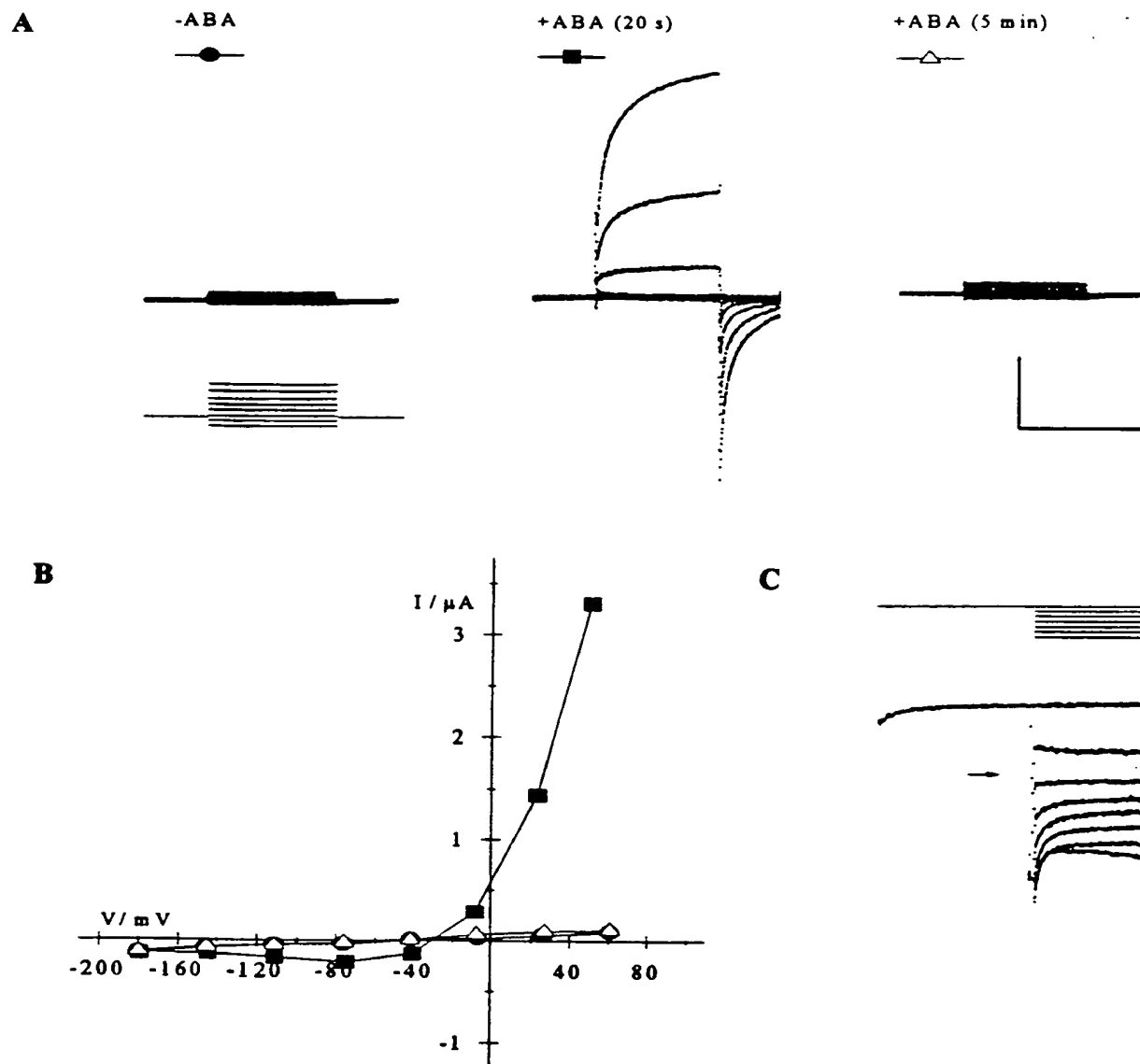


FIG.16

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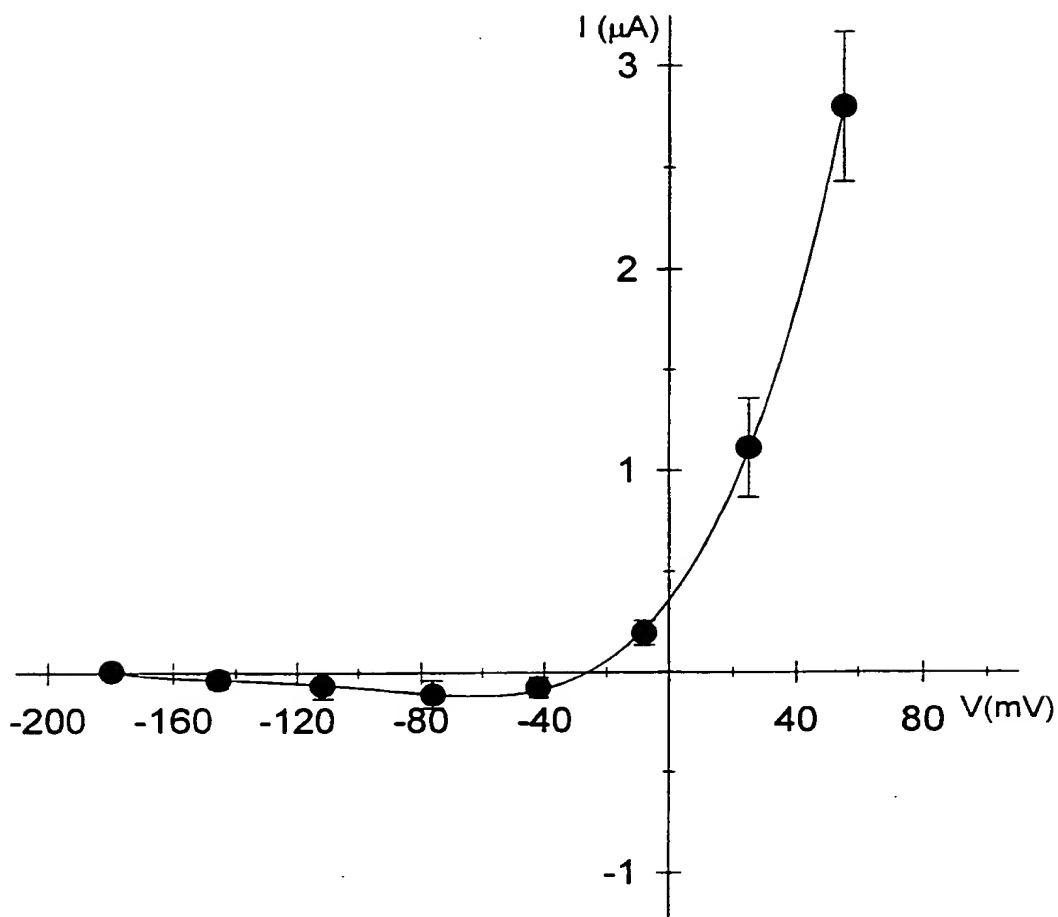


FIG. 17

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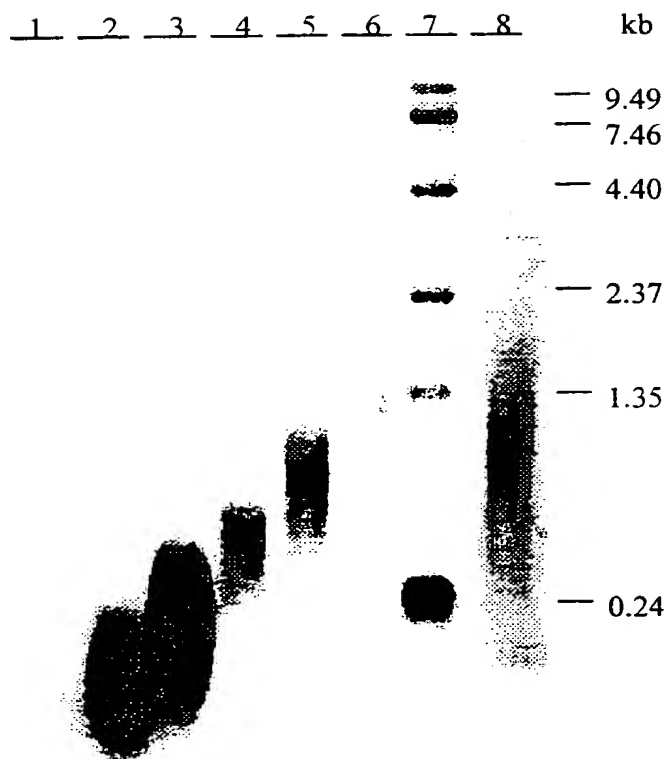


FIG. 18

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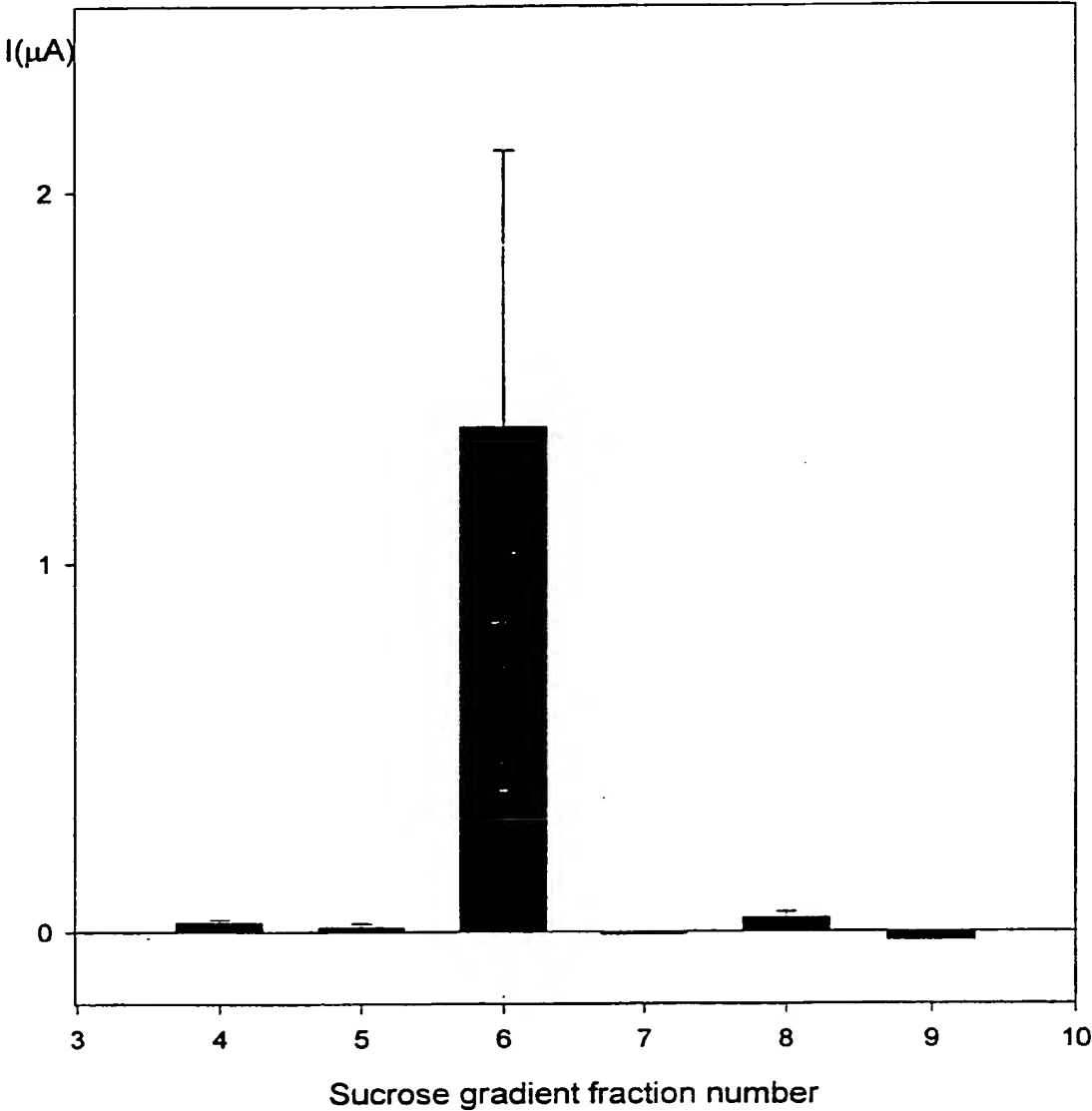


FIG. 19

APPROVED	O.G. FIG.	
BY	CLASS	WO 99/16880
DRAFTSMAN		

09/509738
PCT/GB98/02937

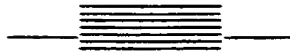
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Pool size

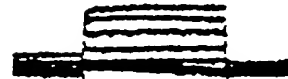
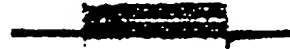
- ABA

+ ABA

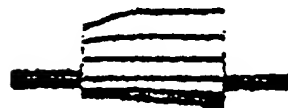
20000



2000



200



20

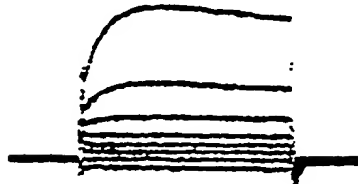
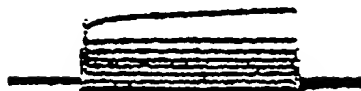


FIG. 20

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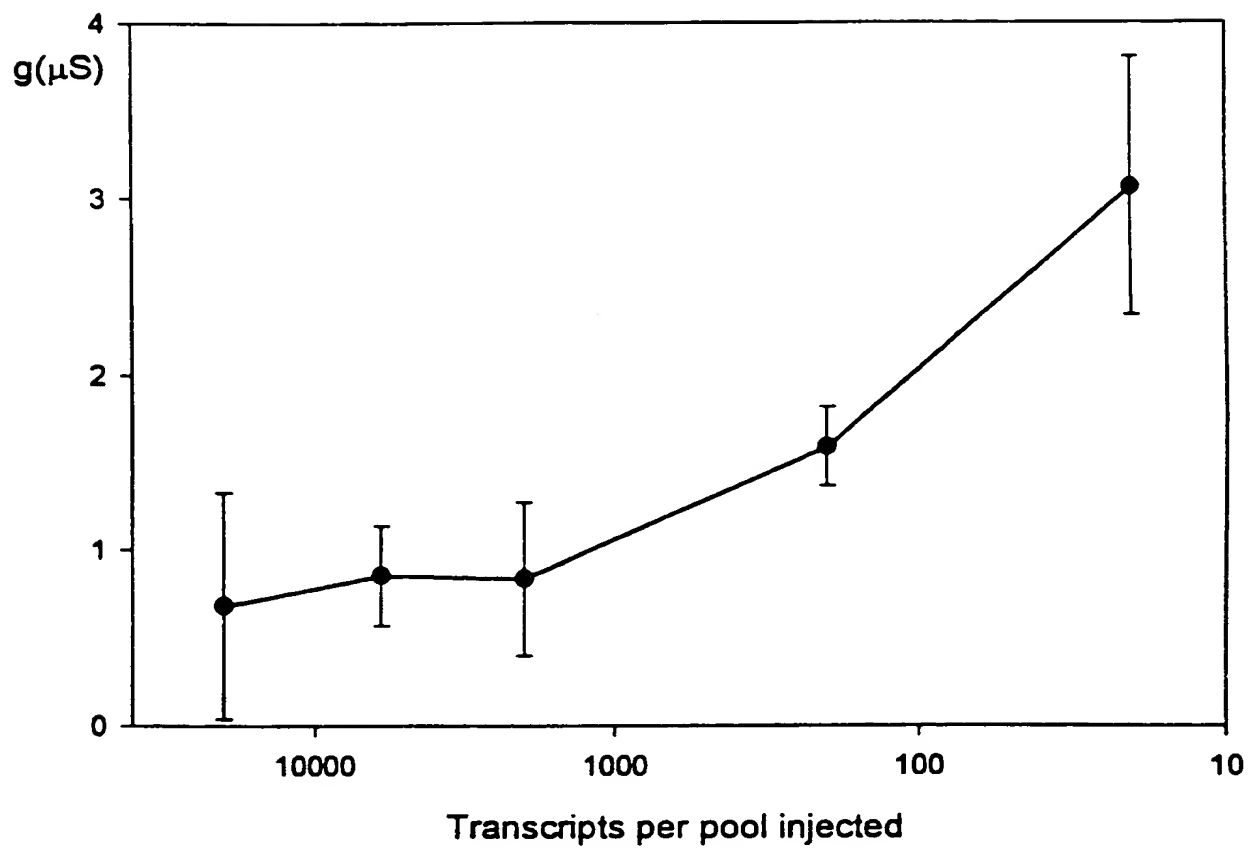


FIG. 21

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	WO 99/16880	

09/509738

PCT/GB98/02937

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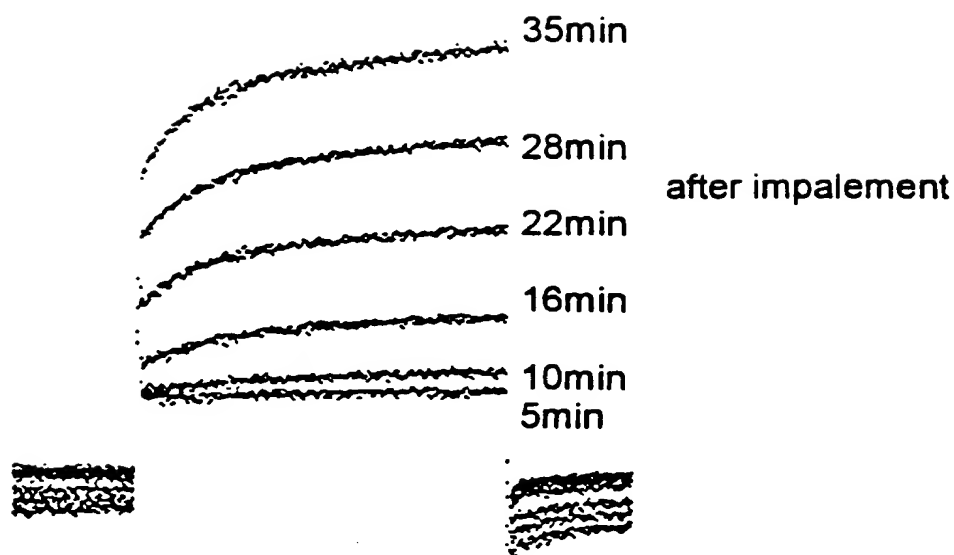


FIG. 22

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A

2.5 mM K⁺

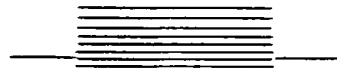
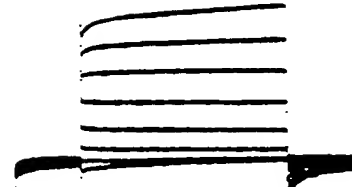
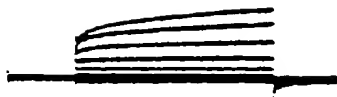
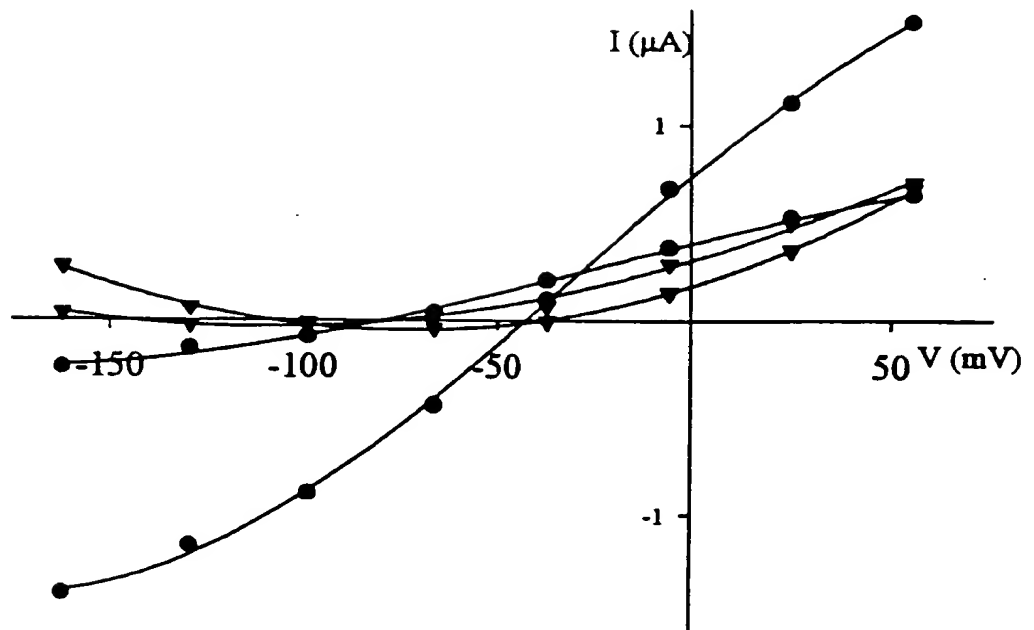
25 mM K⁺

B


FIG.23

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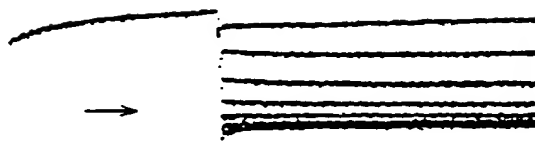
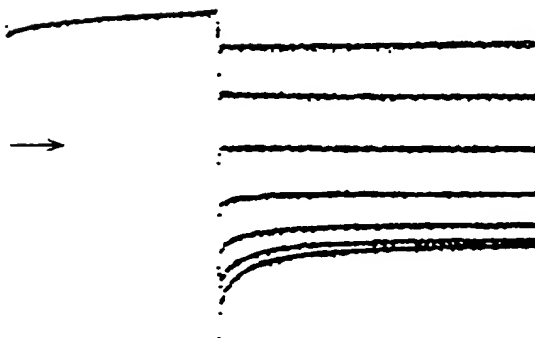
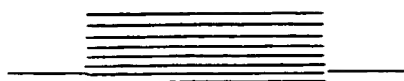
2.5 mM K⁺25 mM K⁺

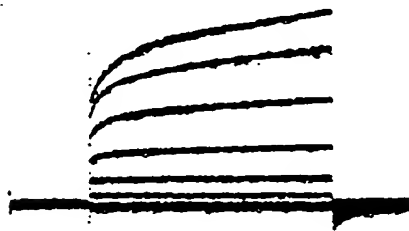
FIG. 24

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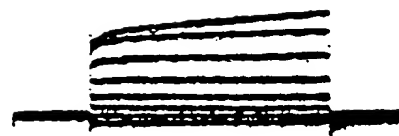


control

TEA



Ba²⁺



Niflumic Acid

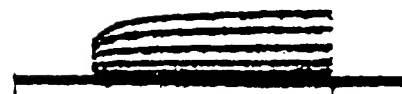
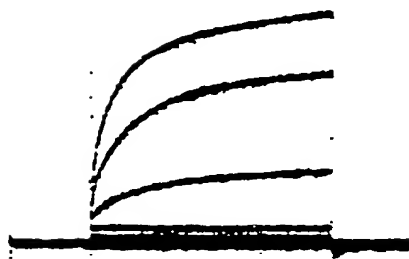


FIG. 25

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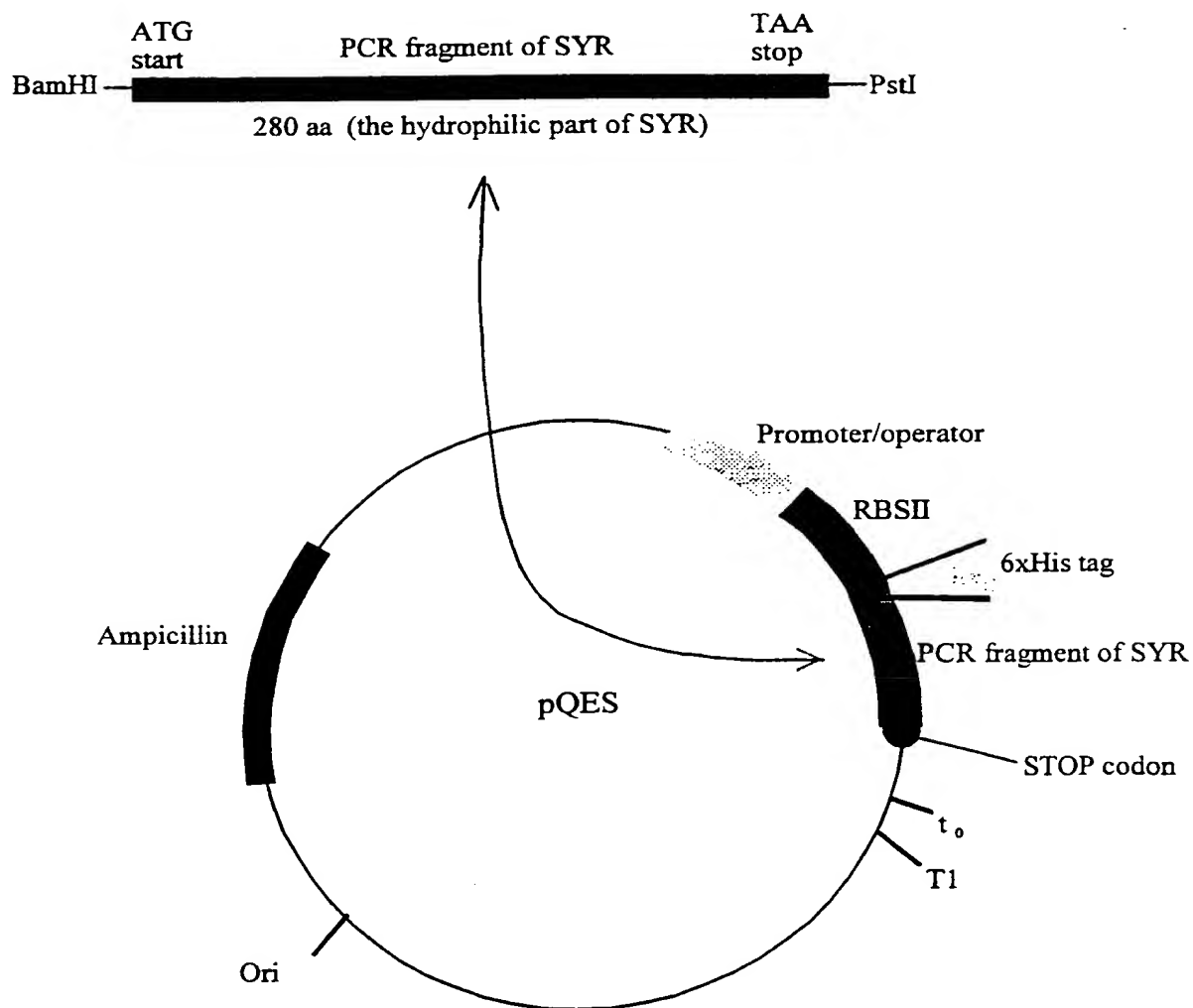


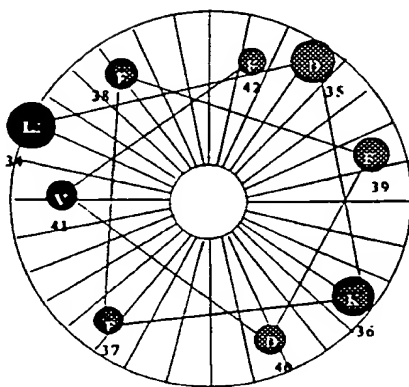
FIG. 26

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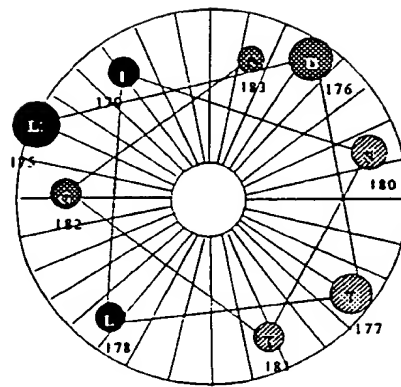
FIG. 27

- A.
- | | |
|--------|----------------------------------|
| LQVARK | SYR-Nt |
| TKKALK | syntaxin 1A-DRO |
| TKKAVK | syntaxin 1A-RAT, syntaxin 1A-HUM |
| TDKAVK | SSO1-yeast |
| TNKAVK | SSO2-yeast |

B.



X1



X2

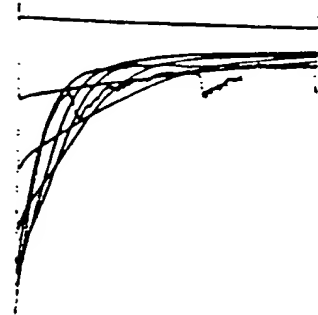
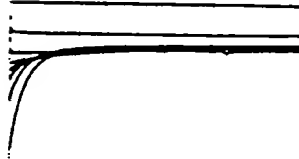
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A.



Contr -ABA

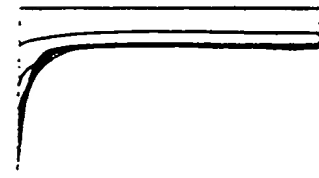
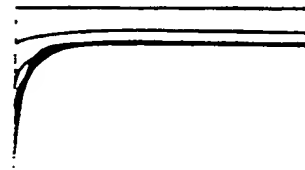
Contr +ABA



B.

BotC -ABA

BotC +ABA



C.

BotD -ABA

BotD +ABA

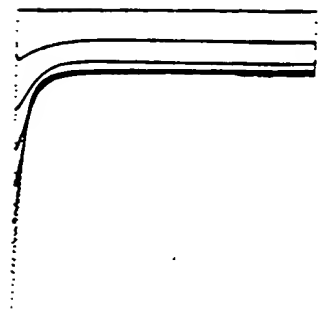
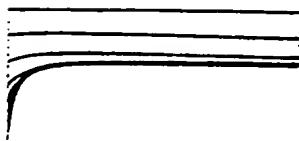
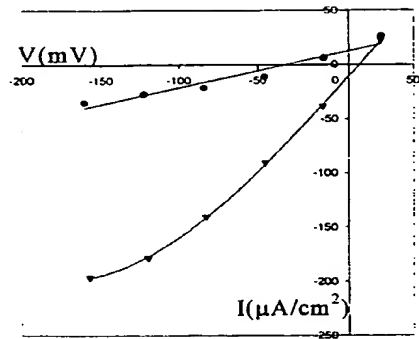


FIG. 28

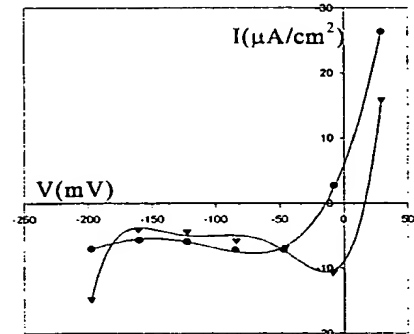
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A.

Contr inst

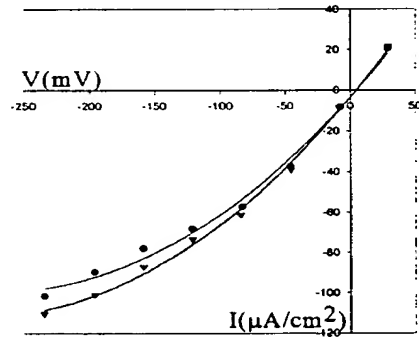


Contr St-St

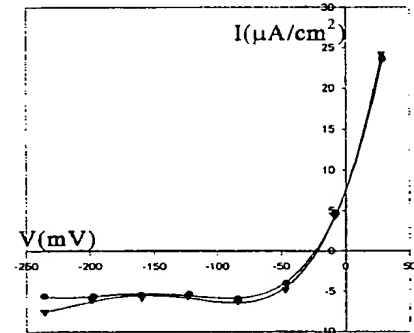


B.

BotC Inst

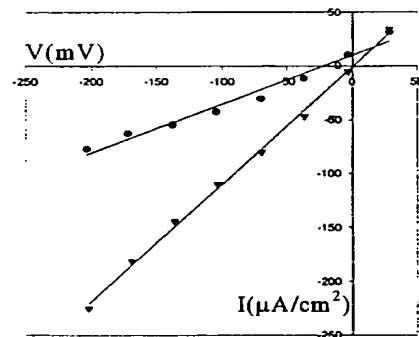


BotC St-St

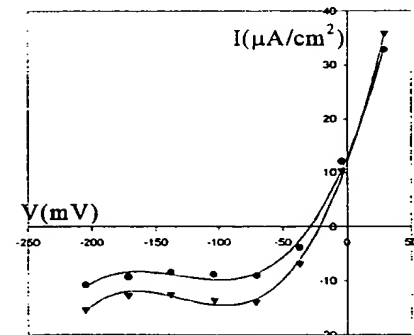


C.

BotD Inst



BotD St-St



• -ABA
▼ +ABA

FIG. 29

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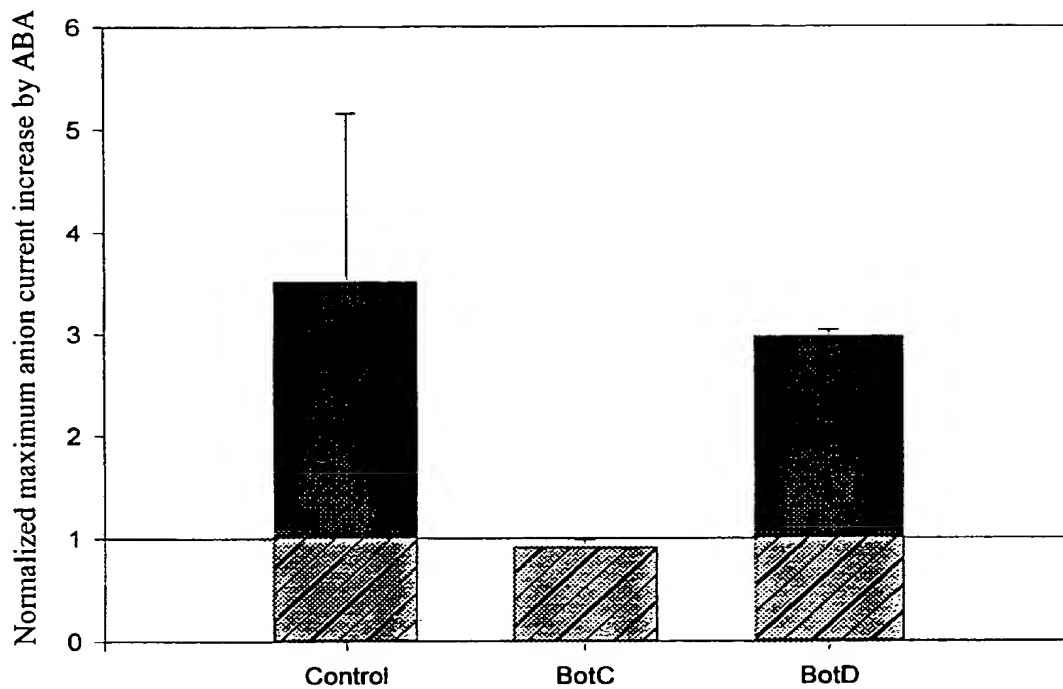
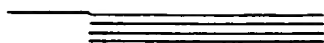


FIG. 30

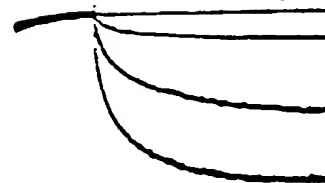
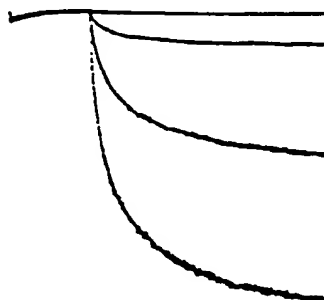
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A.



Contr -ABA

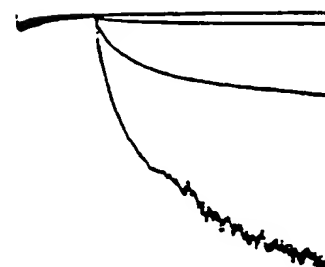
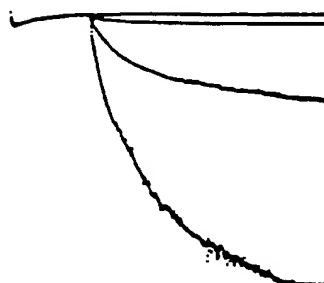
Contr +ABA



B.

BotC -ABA

BotC +ABA



C.

BotD -ABA

BotD +ABA

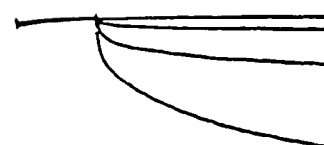
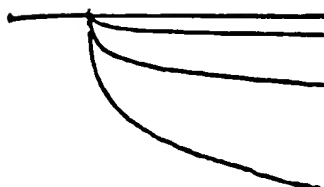
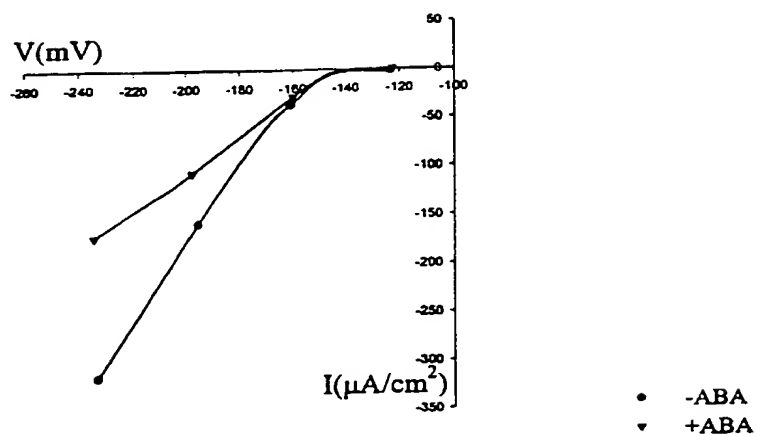


FIG. 31

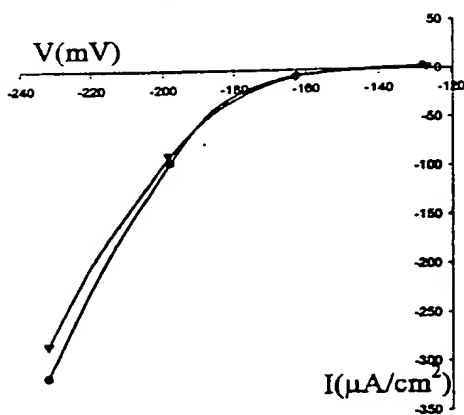
004250-32250360

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A.

Contr St-St K_{in}


B.

BotC St-St K_{in}


C.

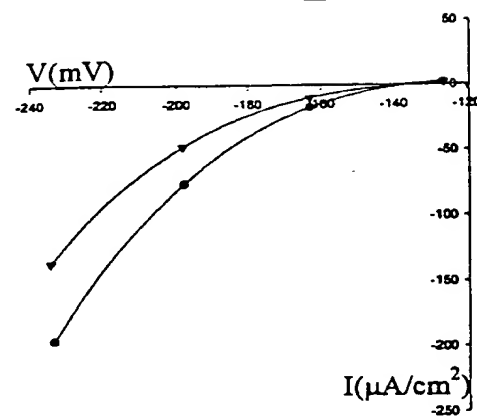
BotD St-St K_{in}


FIG. 32

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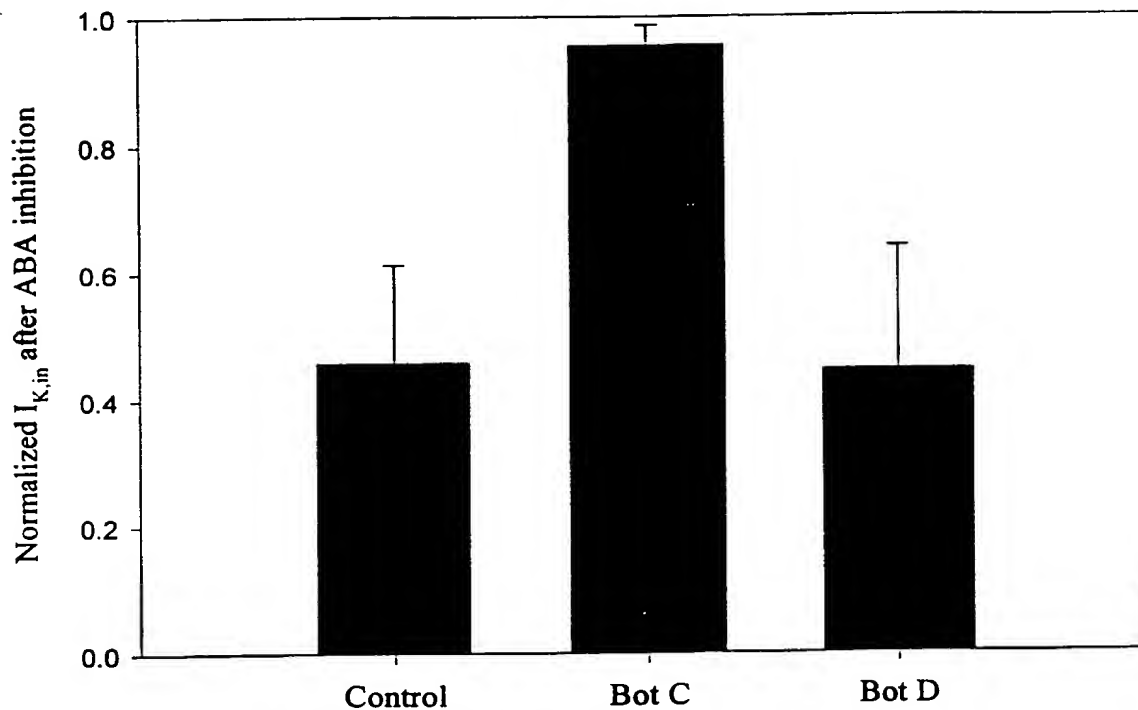


FIG. 33

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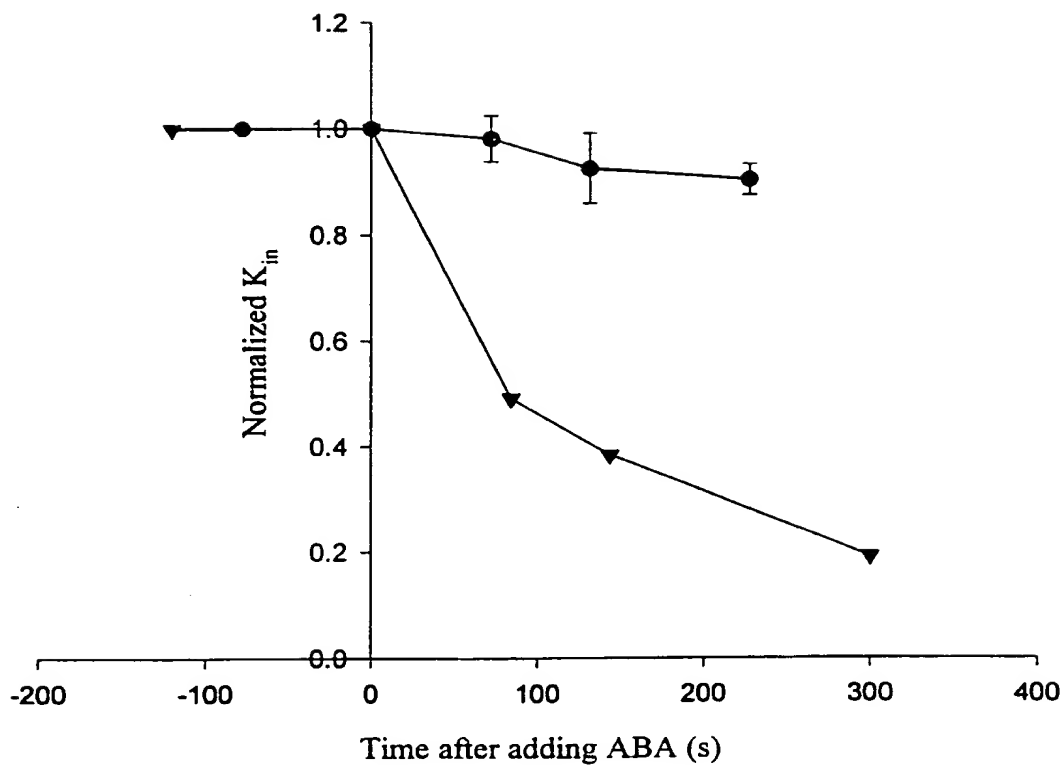


FIG. 34

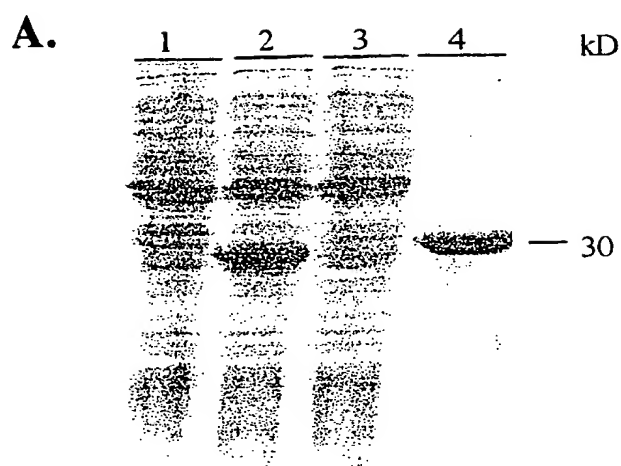
APPROVED	C.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	WO 99/16880	

09/509738

PCT/GB98/02937

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FIG. 35



B.

1	2	3	4
			

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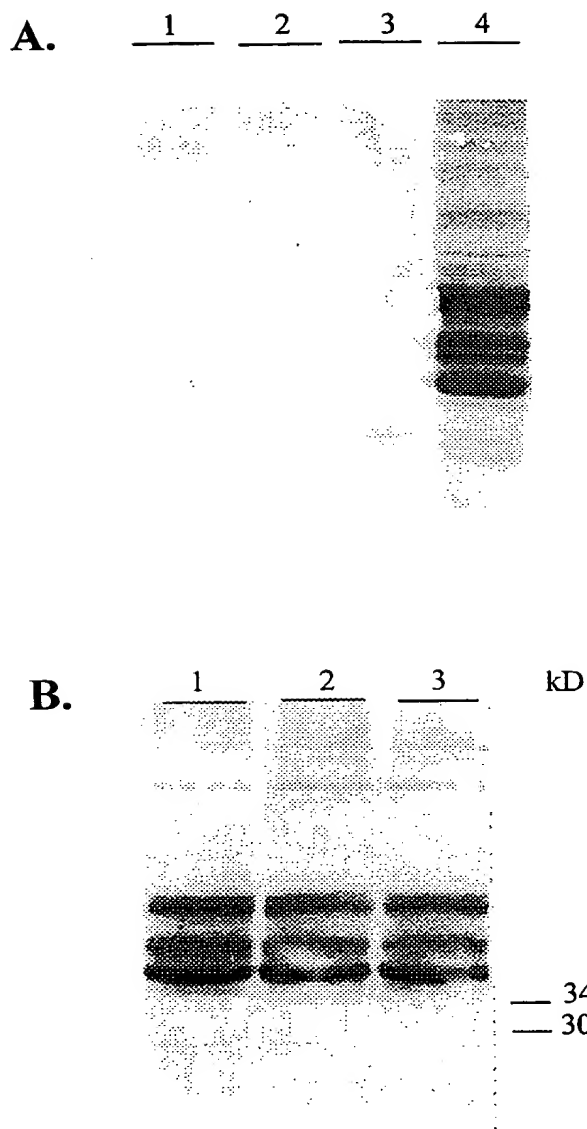


FIG. 36

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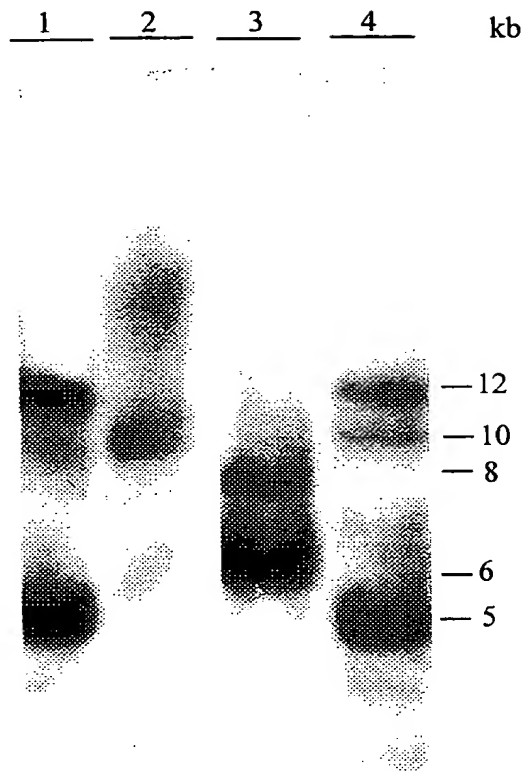
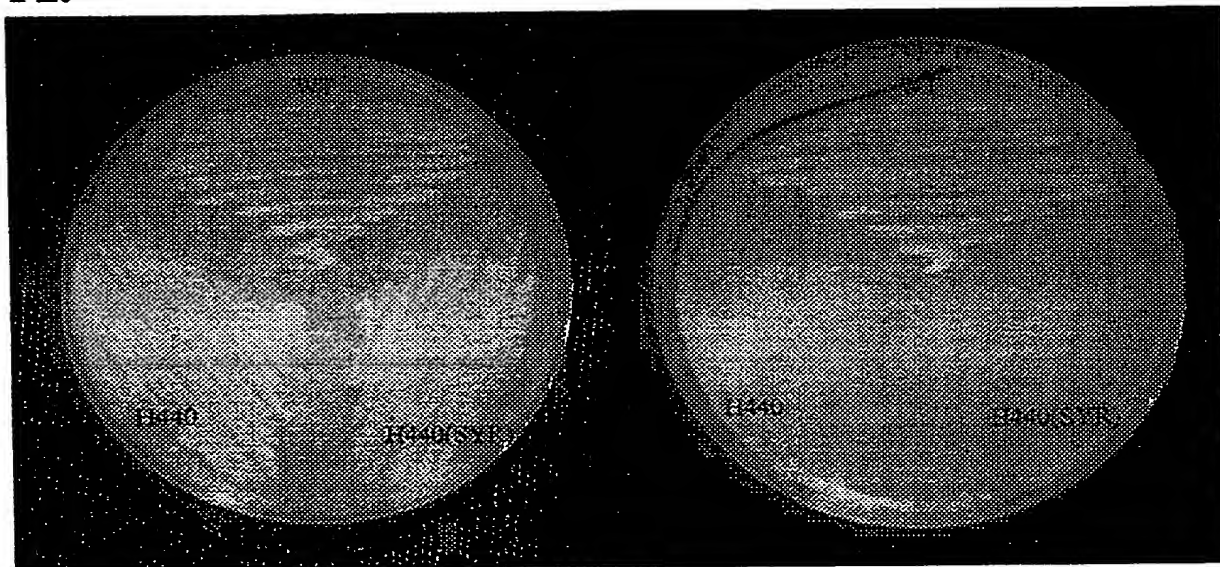


FIG. 37

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A.

B.



C.

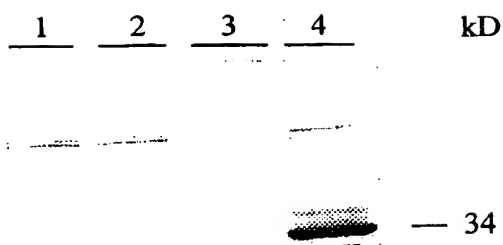


FIG. 38

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	WO 99/16880	

09/509738
PCT/GB98/02937

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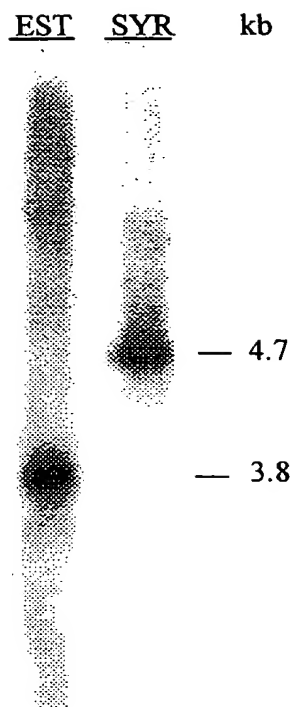


FIG. 39

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	WO 99/16880	

09/509738

PCT/GB98/02937

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TTTAGATTACTCTTATATTAGTTTGTGTTTAAATTGGACGGTTGTTATATCTTTTCTTA
ATATGAGATTTATGTCGTTATTAATGTTTTCTCTTGAGGGTTCATAAAGAGATTTATCGTG
TACCTGGGGGTAGGTCAAATGAGAAGGGGTGTAATTTTGTGTTTTTTTTTAGGTTTTATTGT
GTTTTATTATTCGTACCGATTTTATTATTTTATATTTTAAATCTTATAAGTTTTGTAACCT
CCCCAGGTGGTCTTCTGGAACTGGTATCTGTTTAAAGAGTAAAAAGGTACCGACTTATCTT
TCTTGGTGGTGGTTTTACTACTATTCGTCTTCTTATTATCGTTTTGTTTCAAGGTAAAAGATCA
CAAGAAGACCACGAAGGAACGGTGAACGTCAACGACTCGTGGGGGAGATTGCTTCCTTAATC
GGGATAAGTGAACCGAGAGTTATAGTAGTTCAACTCGAGGAACTGAAAGTTGGTTTTGTCGG
TACAGGTTCTTATGAACACGTTAAGAAAGTTAAGGAGAGGTTAAGGAAGTGTCGAAGTAC
GGAAAGAACTTAAAGGTATTGACATAGGTAGTGAACAGGAGAGGGAACGAGAACCTAACGGA
AAACGTTCTTGACAGAGTGAACTGGACATCTATACTCACATAGTTCTTGACGAAGTAGTCCT
AAAAGAGGACACTGCCATATTATAGCAGCAACTTGACAAAGGGATATAAGTCTACGGTAGAA
AACGGAATCGAGCAACTTGACTAAGTAAGTGAAGAACTTCAAAGAAGGAATTAGGCAAGTGTT
GACTTCAAGAGCAGGACAGTCTACTTGAAGGCCAGGTGTAGGTCCTCCGAAGCTAAGCGA
CGTAAACTAGACAGATTCCGAAGCTCTGCTTGAACTACTTAAACCGAAAGAAGTTACGGTA
CCTTTGCAGTAATAGGTACAACCTAGAATCTAGAAATTGCCGAAATCGCAACACTTCTCAGA
ACGAAAAAAGTACCCTTCTAACCTCAACCCTTATCTAAAAGAGCTCCGGAACCTCAAGCAGA
AATTACCGAAGTTGTAGAAGCTTCTTAAACAGCTCTAACTGAGGCGGTCATTACAGAGGGTA
AAGATACCGCACTCTCAGGCTAACTAGCAGTCGAGACTTTGCTCTCTTTCTAGGACTTTTAT
CTAGTAAGTAAACTCTACCCTAAACC

FIG. 40

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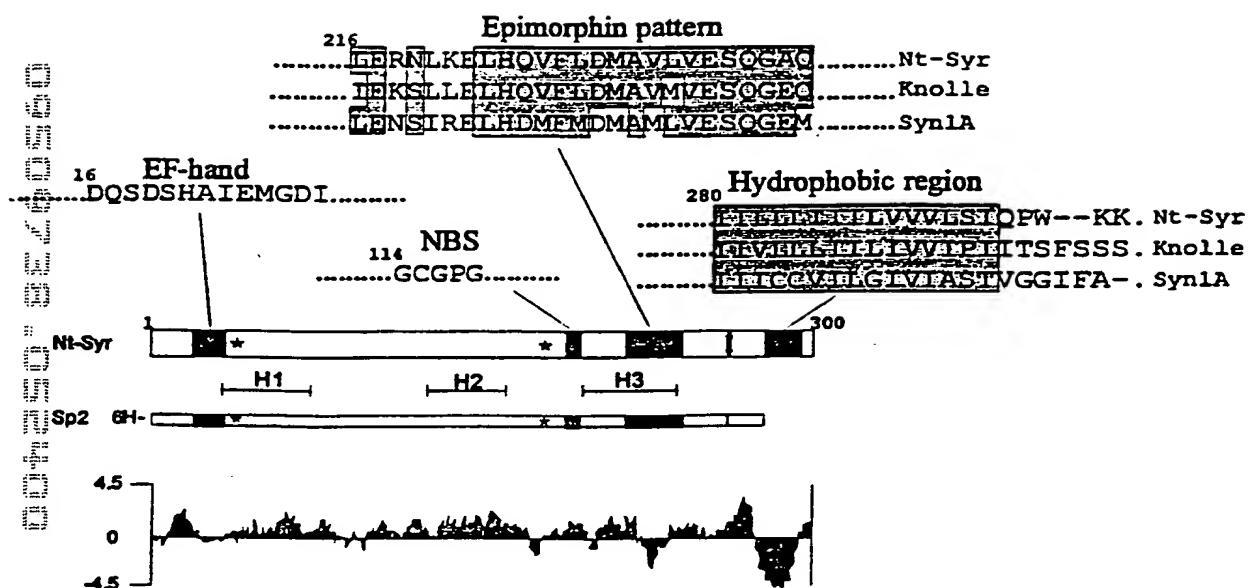


FIG. 41

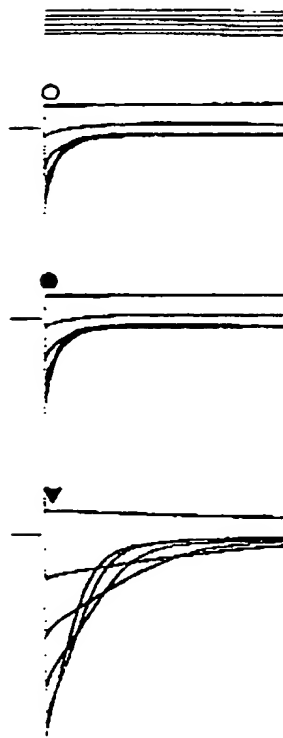
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FIG. 42

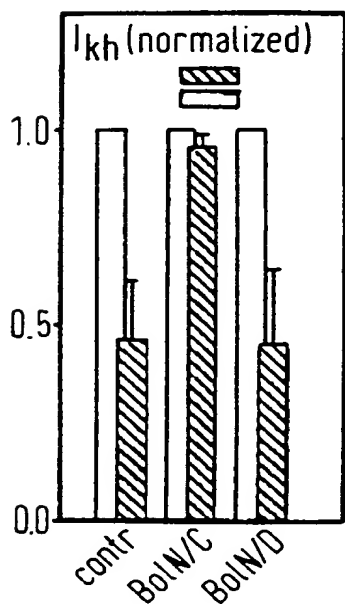
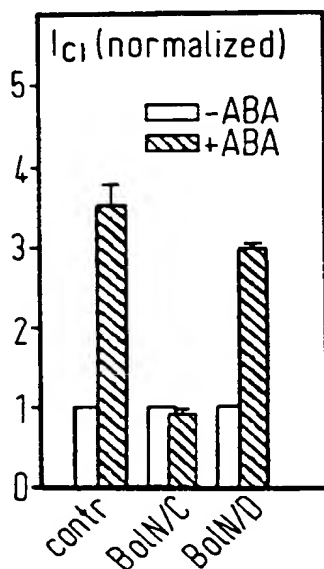
A

Contr	BotN/C	BotN/C	BotN/D
+ATP	+ATP	-ATP	+ATP

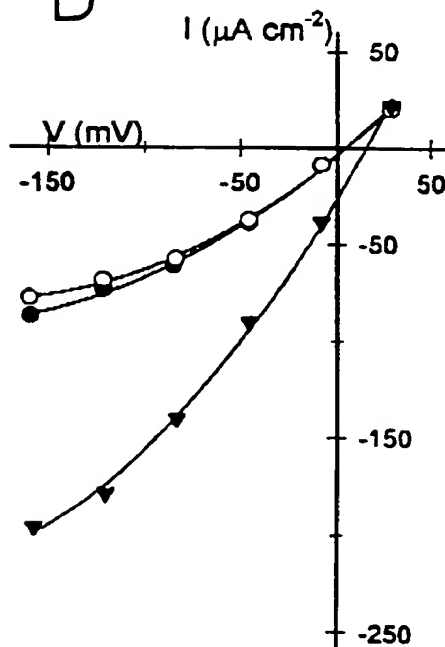
B



C



D



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FIG. 43

